


```

QY      301 CDHRYALNEIYKVKQKTEBDAQKFCFYEQAANVAVSPSEMAVPIIQAOLANIRSKDYK 360
      |||
Db      301 CDHRYALNEIYKVKQKTEBDAQKFCFYEQAANVAVSPSEMAVPIIQAOLANIRSKDYK 360
QY      361 DVKDVEIKQPLLSIELVE 380
      |||
Db      361 DVKDVEIKQPLLSIELVE 380

```

RESULT 2

```

US-09-316-080-5
; Sequence 5, Application US/09316080
; Patent No. 6180366
; GENERAL INFORMATION:
; APPLICANT: John C. Royer
; APPLICANT: Lynne M. Christianson
; APPLICANT: Gregory A. Gambetta
; APPLICANT: Howard Brody
; APPLICANT: Suzanne M. Oclant
; APPLICANT: Wendy T. Yoder
; TITLE OF INVENTION: Methods For Producing Heterologous
; TITLE OF INVENTION: Polypeptides In Trichocheene-Deficient Filamentous Fungal
; FILE REFERENCE: 5563.200-US
; CURRENT APPLICATION NUMBER: US/09/316,080
; EARLIER FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: 09/082,217
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 5
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Fusarium
US-09-316-080-5

```

```

Query Match      95.9%; Score 1966.5; DB 3; Length 377;
Best Local Similarity 96.3%; Pred. No. 5.4e-203;
Matches 366; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY      1 MENPTEYFLNTSVRLLEYIRYDSNTYREERIENLHYAANKAAHFAQPRQOQLKVP 60
      |||
Db      1 MENPTEYFLNTSVRLLEYIRYDSNTYREERIENLHYAANKAAHFAQPRQOQLKVP 60
QY      61 KRLQASLOTTIVGMVYSAKYSKECMADLSHYTYTLVLDSSDDPPYAMNNTYNDLQAG 120
      |||
Db      61 KRLQASLOTTIVGMVYSAKYSKECMADLSHYTYTLVLDSSDDPPYAMNNTYNDLQAG 120
QY      121 REQAHPMWALVNEHFPNVLRFHGFPCSLNLRSTLDFPEGCMIEQYNFGPGSHDYPOF 180
      |||
Db      121 REQAHPMWALVNEHFPNVLRFHGFPCSLNLRSTLDFPEGCMIEQYNFGPGSHDYPOF 180
QY      181 LRRNNGGCHCAGALMPKEQFDERGLFLEITSIAIQEMNMMVAVNDLMSFYKEFDDERDQ 240
      |||
Db      181 LRRNNGGCHCAGALMPKEQFDERGLFLEITSIAIQEMNMMVAVNDLMSFYKEFDDERDQ 240
QY      241 ISLVKNTYVSDERTLHEALEKLTQDTLHSSKQWAVASDDQPOVMDITECMHGTYTWMH 300
      |||
Db      241 ISLVKNTYVSDERTLHEALEKLTQDTLHSSKQWAVASDDQPOVMDITECMHGTYTWMH 300
QY      301 CDHRYALNEIYKVKQKTEBDAQKFCFYEQAANVAVSPSEMAVPIIQAOLANIRSKDYK 360
      |||
Db      301 CDHRYALNEIYKVKQKTEBDAQKFCFYEQAANVAVSPSEMAVPIIQAOLANIRSKDYK 360
QY      361 DVKDVEIKQPLLSIELVE 380
      |||
Db      361 DVKDVEIKQPLLSIELVE 380

```

RESULT 3

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US-08-351-981-2
; Sequence 2, Application US/08351981

```

```

; Patent No. 5589372
; GENERAL INFORMATION:
; APPLICANT: Robinson, Gordon W.
; TITLE OF INVENTION: Squalene Synthetase
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Burton Rodney
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,981
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/911,835
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC7a
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 252-5901
; TELEFAX: (609) 252-4526
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-351-981-2

```

```

Query Match      4.8%; Score 98; DB 1; Length 444;
Best Local Similarity 22.6%; Pred. No. 0.12;
Matches 65; Conservative 36; Mismatches 86; Indels 100; Gaps 15;

QY      70 IYGVNVTYSAKYSKECMALD-----SIHYTYTLVLDSSDDPPYAMNNTYNDLQAGREQAH 125
      |||
Db      45 LNLWTSRSPAVALREHAPBLRNCVTLYLRLALDTIEDD-----MSIEHDKI----- 93
QY      126 PMWALVNEHFPNVLRFHGFPCSLN-----LIRSTLDFPEGCMIEQYNFGPGSHDYPOF 163
      |||
Db      94 -----DLRHFHKLITKMSFDGNAAPDYKDAVLTDFESILIEFHKLKPEYOE 142
QY      164 -----EQYNFGPGSHDYPOF-----LRRNNGGCHCAG 193
      |||
Db      143 VIKETKNGMGADYILDENYNLGLQTVHDYDCHYVAGLVGGLTRLIVIAKFAVE 202
QY      194 SLMPKXEQ-FDERGLFLEITSIAIQEMNMMV-----WANDLMSFY-----KEF-DDERDQIS 242
      |||
Db      203 SLTSEQLTESGLFLEKTNIIIRDYNEEDLVDRSSFWPKIEMQYAPQLDFMKPENEDLG 262
QY      243 L-VKNVYVSDERTLHEALEKLTQ-DTLH--SSKQWAVASDDQPOVM 285
      |||
Db      263 LDCINHLVLA--ALSHVIDVLTLYLSIHQSTFQFCAL-----PQVM 302

```

RESULT 4

```

US-07-861-458C-98
; Sequence 98, Application US/07861458C
; Patent No. 6232061
; GENERAL INFORMATION:
; APPLICANT: Marchionni, Mark Andrew
; APPLICANT: Johnson, Carl D.
; TITLE OF INVENTION: HOMOLOGY CLONING
; NUMBER OF SEQUENCES: 142

```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/861,458C
 FILING DATE: 04/01/92
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 04585/014001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 98:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 753
 TYPE: amino acid
 TOPOLOGY: linear
 US-07-861-458C-98

Query Match 4.8%; Score 97.5; DB 3; Length 753;
 Best Local Similarity 20.3%; Pred. No. 0.32;
 Matches 79; Conservative 41; Mismatches 137; Indels 133; Gaps 22;

QY 5 PTEYPLNTSVRLLEYIRDSNTREERIENTLHY--AYNKAHHFAOPROOQLKNDPKR 62
 DB 69 PSEYMSOVYDPLAYLOETTKFYTEREYEDFGGECFNST-----ESEVQVTPN- 118
 QY 63 LQASLQITGVMMVYS--MAKVSKECMADLSIHYYTYTLVLDSSD-----PY 107
 DB 119 -----VYRAVAVVFLPGCM--IMLYLAOSVLDKRNNEKIYDIQLKPTAPF 165
 QY 108 PAMNMYFNDLQAGREQAHPMWALVNEHFPNVLRFHGF-----CSLNLIRSTLDFFEGCW 162
 DB 166 PAL-----TICNLNLYKASLATSVDLVKRTLSAFDGA- 197
 QY 163 IEQYNGFGFPGSHDYPOFLRRNGLGHCVGASLMPKEQFP-----ERGLPLEITSAIAQM 217
 DB 198 -----MGKAGGNKDHBE--EREFGFARCLGSGSQSSQEDKDEKEBELLETTKKVFN 250
 QY 218 E-----NMWVWVNDLMSFYKEFDERDQISLVKVVYVSDITLHEALEKLTQDTLHSSQ 272
 DB 251 NGECCNMGEMKNKNTWSIMR-----ITWKKQLLEMN--MMEECSEKRNSTSPFG-- 298
 QY 273 MVAVFSDK-----DPQVMDTIECFMHSYVTWHL--CDHRYRLNEIYKVGOKETEDA--- 322
 DB 299 -----FDRRCICAFPRSTHDMPCPLNG--TWETTECD--TCNENHACTDNTAKGHR 349
 QY 323 -----OKFCFYEQAANVGAVSFSE-MAY 345
 DB 350 PCICAPSRFCVAVN-----GKTPRIEIMTY 374

RESULT 5
 US-08-351-981-8
 ; Sequence 8, Application US/08351981
 ; Patent No. 5589372
 ; GENERAL INFORMATION:
 ; APPLICANT: Robinson, Gordon W.

TITLE OF INVENTION: Squalene Synthetase
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burton Rodney
 STREET: P.O. Box 4000
 CITY: Princeton
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 08543-4000
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/351,981
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/911,835
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Gaul, Timothy J.
 REGISTRATION NUMBER: 33,111
 REFERENCE/DOCKET NUMBER: DC7a
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (609) 252-5901
 TELEFAX: (609) 252-4526
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-351-981-8

Query Match 4.7%; Score 97; DB 1; Length 444;

Best Local Similarity 21.9%; Pred. No. 0.15; Matches 63; Conservative 37; Mismatches 86; Indels 102; Gaps 15;

QY 70 IGVGVVYVMAKVSKECMADL-----SIHYTYTLVLDSSDDPYPMNMYFNDLQAGREQAH 125
 DB 45 LMDTGRSPAAVYRELHPELRNCVTLYLLRLADTIEDD-----MSIEHDLKI----- 93
 QY 126 PMWALVNEHFPNVLRFHGFCSLN-----LIRSTLDFFEGCW----- 163
 DB 94 -----DLRHFHEKLLTKWSFDGNADVDKRAVLTDFFESILIEFHKLKPEYQE 142
 QY 164 -----EQYNGFGFPGSHDYPOFLRRNGU-----GHCVGA 193
 DB 143 VIKETKMGNGMADYILDENYVNLGLQVHDYKVCYVAGLVGDLIRLIYANFANE 202
 QY 194 SLMPKEQ-FDERGLPLEITSAIAQEMNMY-----WVNDLMSFY-----KEF-DDERDQIS 242
 DB 203 SLYSNEOLYESMGLFLOKNTIIRDYNEEDLVGDSFMPKEIWSGYAQLQDFMARENEQLG 262
 QY 243 L--VKVVYVSDITLHEALEKLTQ-DTLH--SSKQWVAVFSDKDPQVM 285
 DB 263 LDCINHLVIN--ALSHVIDVLTYLASIHGQSTFOFCAI-----PQVM 302

RESULT 6
 US-08-468-558-2
 ; Sequence 2, Application US/08468558
 ; Patent No. 5877280
 ; GENERAL INFORMATION:
 ; APPLICANT: Wetmur, James G.
 ; TITLE OF INVENTION: Cloning and Expression of Thermostable
 ; TITLE OF INVENTION: Muts Genes and Proteins and Uses Therefor
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

```

/ STREET: Two Militia Drive
/ CITY: Lexington
/ STATE: Massachusetts
/ COUNTRY: United States of America
/ ZIP: 02173
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,558
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Granahan, Patricia
/ REGISTRATION NUMBER: 32,227
/ REFERENCE/DOCKET NUMBER: MSM94-05
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-861-9540
/ TELEFAX: 617-861-9540
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 855 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-468-558-2

```

```

Query Match      4.5%; Score 92.5; DB 2; Length 855;
Best Local Similarity 19.4%; Pred. No. 1.3;
Matches 75; Conservative 58; Mismatches 118; Indels 135; Gaps 20;

QY 12 TSVRLLEYIRYDSNYTREERIENLHYANKAAHFAAPROOQLKVPKQLQASLQITV 71
DB 512 TRINLEYELVRE--LREEVKELDKVGNNA-----TLI 543

QY 72 GNVVY-----SWAKVSKECMADLSIHYYTLVLDDSSDDPYPM---MNYF-NDLOAGRE 122
DB 544 GEVDYIQLSLAMLEKGMVPR-EVHEGYELIIEGK---HPVIEFTKYNVPNDTK---- 595

QY 123 QAHFWALVNEHFPNVLRHFGPFCSLNLRSTLDFEGCGWIEQYNFGFPGSHDYPOFLR 182
DB 566 -----LTEEFHIVIT--GP-----NMAGKSSYIRQYG 621

QY 183 RMNGLHCVCASLMPKEQFDERGLFLETGSAIAQWENMM---VMVNDLMSF-YKEPDDR 238
DB 622 VLTLLAH-----TGSFLPKSARIPVDALFTRIGSDVLAGVSTFMNEM 667

QY 239 DOISLVKN-----YVSDETLHEALEKLTQDTLHSSKQWAVFSDKPOVMQDTECFM 292
DB 668 LDVSNLNATKRSLLIIDEVGRGTS---TYDGIASIKAIKVIYSEK----- 711

QY 293 HGVTWMLCDHRVRLNEIYEKVG-----QKTEDAQKCFKFEQAANVAVSPSEWA 344
DB 712 IGAKTL-LATHYLELTELERRKVGKVGNYHMEVEETDEGIRFLYILKEGAKSGFQID--- 767

QY 345 YPPIAQLANIRSKDVQDVV-KEIQ 369
DB 768 ---VAKLAGLPEEVAREAKIKLELE 790

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RESULT 7
US-08-676-444-2
/ Sequence 2, Application US/08676444A
/ Patent No. 6294325
/ GENERAL INFORMATION:
/ APPLICANT: Metmur, James G.
/ TITLE OF INVENTION: CLONING AND EXPRESSION OF THERMOSTABLE
/ FILE REFERENCE: MSM95-02
/ CURRENT APPLICATION NUMBER: US/08/676,444A
/ CURRENT FILING DATE: 1996-07-05

```

```

/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 855
/ TYPE: PRT
/ ORGANISM: Aquifex pyrophilus
US-08-676-444-2

```

```

Query Match      4.5%; Score 92.5; DB 3; Length 855;
Best Local Similarity 19.4%; Pred. No. 1.3;
Matches 75; Conservative 58; Mismatches 118; Indels 135; Gaps 20;

QY 12 TSVRLLEYIRYDSNYTREERIENLHYANKAAHFAAPROOQLKVPKQLQASLQITV 71
DB 512 TRINLEYELVRE--LREEVKELDKVGNNA-----TLI 543

QY 72 GNVVY-----SWAKVSKECMADLSIHYYTLVLDDSSDDPYPM---MNYF-NDLOAGRE 122
DB 544 GEVDYIQLSLAMLEKGMVPR-EVHEGYELIIEGK---HPVIEFTKYNVPNDTK---- 595

QY 123 QAHFWALVNEHFPNVLRHFGPFCSLNLRSTLDFEGCGWIEQYNFGFPGSHDYPOFLR 182
DB 566 -----LTEEFHIVIT--GP-----NMAGKSSYIRQYG 621

QY 183 RMNGLHCVCASLMPKEQFDERGLFLETGSAIAQWENMM---VMVNDLMSF-YKEPDDR 238
DB 622 VLTLLAH-----TGSFLPKSARIPVDALFTRIGSDVLAGVSTFMNEM 667

QY 239 DOISLVKN-----YVSDETLHEALEKLTQDTLHSSKQWAVFSDKPOVMQDTECFM 292
DB 668 LDVSNLNATKRSLLIIDEVGRGTS---TYDGIASIKAIKVIYSEK----- 711

QY 293 HGVTWMLCDHRVRLNEIYEKVG-----QKTEDAQKCFKFEQAANVAVSPSEWA 344
DB 712 IGAKTL-LATHYLELTELERRKVGKVGNYHMEVEETDEGIRFLYILKEGAKSGFQID--- 767

QY 345 YPPIAQLANIRSKDVQDVV-KEIQ 369
DB 768 ---VAKLAGLPEEVAREAKIKLELE 790

```

```

RESULT 8
US-09-710-279-2362
/ Sequence 2362, Application US/09710279
/ Patent No. 6703492
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: P0348005
/ CURRENT APPLICATION NUMBER: US/09/710,279
/ PRIOR FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: 60/164,258
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 2362
/ LENGTH: 602
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-09-710-279-2362

```

```

Query Match      4.5%; Score 92; DB 4; Length 602;
Best Local Similarity 18.5%; Pred. No. 0.87;
Matches 74; Conservative 49; Mismatches 120; Indels 156; Gaps 20;

QY 19 YIRY--RDSNTYREERIENLHYA-----NKAHFAAPROOQL 56
DB 204 FKITYESDRRLASAFRNVYKAGANNITGATLAGEVKKVFNARTTHYRSARERALS 263
QY 57 KVD-PKRLQASLQITVGM---VYVSWAKVSKCMA--DLSIHYYTL-LVLDDSSDDPYPA 109

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Db      264 NNHIFPENVNLTXTNHYPLRLHRYTKLAEGLLDLMDYTLTVLVADVKEEMYY-- 321
Qy      110 MNNYFNDLQAGREOAHFWMALVNEHPNVLRHFGPFC--LNLIRSTLDFEGCWIEOYN 167
Db      322 -----EBAKSW-----MLKALEPMEBEYLVNVEKESGLD--NRWVDVYE 356
Qy      168 FGFPFSGHDYPOPLRRNNGI--GHCVGASLMPKEQDERGLPLEITSALAQEMNNWVY 224
Db      357 NKG-----KRSGGYSSGGHLTNPFI-----LNLMSDTV 384
Qy      225 NDLMSPYKEFD-----DERDOI SLVKNYV-----SDE--- 252
Db      385 SDLYTLVHERGSHASYSFQNOPSNLSDYTI FVAEVASTCNEALLSDYMDKLDDEERL 444
Qy      253 ITLHEALEKLTOTLHSSKQMVAVFSDKDPQVMDTIECFMNGYVYVHLCRHYRLNEIYE 312
Db      445 LLLNOELERFRATLFRQT--MFAEFBKHIQIEBAGEPLTPN-----RMNEEYA 491
Qy      313 KVK-----GOKTEDAQKCKEYEQAAVNAVSPSEWAPP 347
Db      492 KLNKLIFYEAEVETDDISK-----EWSRIP 516

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RESULT 9

```

US-09-134-001C-4028
; Sequence 4028, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4028

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Query Match 4.5%; Score 92; DB 3; Length 612;
 Best Local Similarity 18.5%; Pred. No. 0.89;
 Matches 74; Conservative 49; Mismatches 120; Indels 156; Gaps 20;

```

Qy      19 YIRY--RDSNYTREERIENLHAY-----NKAHHFAQPRQOQL 56
Db      214 FIKYLSDDRELASAFRNYKAYGAHNTLTGATLAGEVKKGVFNATHYRSARERALS 273
Qy      57 KVD-PKRLQASLQTIYGM--VYISMAKSKCECA--DLSIHITYT-LVDDSSDDPYRA 109
Db      274 NNHIFPENVNLTXTNHYPLRLHRYTKLAEGLLDLMDYTLTVLVADVKEEMYY-- 331
Qy      110 MNNYFNDLQAGREOAHFWMALVNEHPNVLRHFGPFC--LNLIRSTLDFEGCWIEOYN 167
Db      332 -----EBAKSW-----MLKALEPMEBEYLVNVEKESGLD--NRWVDVYE 366
Qy      168 FGFPFSGHDYPOPLRRNNGI--GHCVGASLMPKEQDERGLPLEITSALAQEMNNWVY 224
Db      367 NKG-----KRSGGYSSGGHLTNPFI-----LNLMSDTV 394
Qy      225 NDLMSPYKEFD-----DERDOI SLVKNYV-----SDE--- 252
Db      395 SDLYTLVHERGSHASYSFQNOPSNLSDYTI FVAEVASTCNEALLSDYMDKLDDEERL 454
Qy      253 ITLHEALEKLTOTLHSSKQMVAVFSDKDPQVMDTIECFMNGYVYVHLCRHYRLNEIYE 312
Db      455 LLLNOELERFRATLFRQT--MFAEFBKHIQIEBAGEPLTPN-----RMNEEYA 501

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Qy      313 KVK-----GOKTEDAQKCKEYEQAAVNAVSPSEWAPP 347
Db      502 KLNKLIFYEAEVETDDISK-----EWSRIP 526

```

RESULT 10

```

US-09-583-110-4076
; Sequence 4076, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PAT00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4076
; LENGTH: 1463
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4076

```

Query Match 4.5%; Score 92; DB 4; Length 1463;
 Best Local Similarity 19.6%; Pred. No. 3.6; Indels 130; Gaps 23;
 Matches 91; Conservative 67; Mismatches 177;

```

Qy      1 MENPTEYFLNTSVRLLEYRY--RDSNYTREERIENLHAYNKAHHFAQPRQOQLKV 58
Db      306 MNNFTDLTMNVQ--DLQEVVHYERKOLMPEGERVE--FRAHNTMSTMDLFEVEIVAT 362
Qy      59 DPR-----RLQASLQTIYGM-----VYISMAKSKEC 85
Db      363 AAKMGKAAVAITDHGVQSEFPHGYKAAKAGIOLIGMEANIVEDRVPIYN--EV 416
Qy      86 MADLSIHITYTLVDDSSDDPYRAMNYPNDLQAGR-----EQAHFPMWA-- 129
Db      417 EMDLS--EATYVVFVETGTSATYNDLIGVAAASKYKGVNVAERDEFINPCHPSAFT 473
Qy      130 -----LVNEHFPN-----VLRHFGPFC--SINLIRSTLDFEGCWIEOYNFGFPGSHDY 177
Db      474 TELTGITDHDVNAKAKLEQLQEFQFCQDTVLVAHNATFDVGFMANVY-----RHDL 527
Qy      178 P-----QFLRM-----NGLGHCV--GASLMPKEQDERGLPLEITSALAQME 218
Db      528 PKISQVIDTLBPARMLYPRYKRGHGLTKRPGVAL--EHHMANYDAEATGRLL-- 581
Qy      219 MNNWVNDLMSFKKEDDERDOI SLVKNYVNSDEITLHEALEKLTOTLHSSKQMVAVFS 278
Db      582 --EPIKEVAERKGVTDLALNTDLISPSYKKAIRKHAITYVKNQGLKNIRFLVSLN 639
Qy      279 DK-----DPOVMOTI--ECFMHGYVYVHLCRHYRLNEIYEKVGOKTEDAQKCKEYEQAA 333
Db      640 TKYFEGVPRPRVLDNAHREGILGSACSE--GAVFDVYVQGVDAVAEVAKYID-- 692
Qy      334 NCVASPSSEWAPPRIAQLANIRSKDVYKDVKEIKPLLSIEL 378
Db      693 FIVMPPAIIYA-PLIAK-----EQVDMELQTIKSLIEV 727

```

RESULT 11

```

US-09-538-092-601
; Sequence 601, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic

```

APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurateSeqFormatter Version 0.9
SEQ ID NO 601
LENGTH: 880
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YML099C
US-09-538-092-601

Query Match 4.5%; Score 91.5; DB 4; Length 880;
Best Local Similarity 19.0%; Pred. No. 1.8;
Matches 80; Conservative 67; Mismatches 127; Indels 147; Gaps 23;

QY 34 ENLHYAVYKAAHFAQPRQQL-----KVDPRKLUAS-----LQTVG 72
DB 307 QNLKLLFOKSSNSBEPRPOLIDDVFNIEPRSLPADLAKITLAPNERRPKSMLE 366
QY 73 MVTYSMAKVSKECM-----ADLSIHYTVTLVLDSSDPYPMNMYFNDLQAGRE---Q 123
DB 367 LITSYS-SDLPELVLDIIPKTDLTWGLARFLLN-----HYFNNAVADKMTVVYLE 414
QY 124 AHPMALVNEFPVNLHFGPCSLN-----LIRSL-----DF 157
DB 415 KNPFKTL--YFPRLMALGLDLAGCGSSNSRNALLNALVSCFHLQSKYPRNYKQY 471
QY 158 FEGCMIEOYNGCGPFGSHDYQPLRMNGLGHCVGASLWPKQEPDERGLFLEITSATQW 217
DB 472 FLGIGIEIRN-----QASNFLCLANT-----KSLPEK--YQDVLTALISM 511
QY 218 ENMWVAVNDLMSFYKEPDERDQISLVKNY-----VSDEI-TLHEALE--KLTPD 265
DB 512 -----NSIDVVGTMADQDHLALCEDFVESRMKLRPNISEKTKTLHRIFSLKLIQD 564
QY 266 TLH-----SSQCMVAVFDKDP--QVMDT-----ICFPHGYVTWILCHRRRLN 308
DB 565 STALDKVRAKEIVLPSEEDNYKPLDTSNATSSSEPRDVVQEG-----FREALN 617
QY 309 EIVEKVGQKTEQKFCCKFY-EOAANYGAVSPSEWAVPPIAOLANIRSKDVKDVKE 367
DB 618 E-----NDCKIHIEFVKEPTIVNSADSTPSSTTPPL--PTNLTATESYVYKSDISK 665
QY 368 I 368
DB 666 L 666

RESULT 12
US-08-826-267-2
Sequence 2, Application US/08826267
Patent No. 5994070
GENERAL INFORMATION:
APPLICANT: Streuli, Michel
TITLE OF INVENTION: NO. 5994070el TRIO Molecules and Uses Related Thereto
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,267
FILING DATE: 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,214
FILING DATE: 27 MARCH (1996)
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2860 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-826-267-2

Query Match 4.4%; Score 90.5; DB 2; Length 2860;
Best Local Similarity 20.7%; Pred. No. 15;
Matches 57; Conservative 37; Mismatches 80; Indels 101; Gaps 11;

QY 202 DERGLFLEITSATIAQ-----MENMMVWVN-----DLMSFYKEPDRS-----RDOISLV 244
DB 379 DERSTLDMSSITRHOAKETKMSVNDKSCAKGCVLDLPSELQDEBDALINHHQIGYEITTLA 438
QY 245 KNYVSDDEITLHBALEK-----LTPDTLSSKOM----- 273
DB 439 YSEVSGQSKLIDKLRPLRGSSDSLTAANYSKAVNHVLDVINEVLHQRVYRTIMQW 498
QY 274 -----VANPSDKDPOYMDTIECFPHGYVTWIL-----CHRRYLL--NEIYKVK 315
DB 499 RKYRLHQRLOLCVFOQEVQVLDIMENHGEAFLSKTKGVKSLRRALQKRHEDEEVA 558
QY 316 GQKTEPAQKFCRYEOAANYGAVSPSEWAVPPIAOLANIRSKDVK----- 361
DB 559 QNTYTNADKLLBAEGLAQGECDPE-----IYQAAHQDEBRIQDPVVRVQKILDM 613
QY 362 -----VKD-----VKEIQKPL-----SSIELVE 380
DB 614 SVSFHTHVKELMTWLELQKELLDVYASVEAVQ 648

RESULT 13
US-09-946-678-2
Sequence 2, Application US/09946678
Patent No. 6541236
GENERAL INFORMATION:
APPLICANT: ITO, Kotaro
APPLICANT: UMITSUKI, Genryou
APPLICANT: KOYAMA, Yasuji
TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
FILE REFERENCE: 0283-0158P
CURRENT APPLICATION NUMBER: US/09/946,678
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: JP 2000-270371
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 2
LENGTH: 684
TYPE: PRT
ORGANISM: Cryptococcus nodaeensis
US-09-946-678-2

	Query Match	19.3%	Score 89	DB 4	Length 324	
	Best Local Similarity	19.5%	Pred. No. 0.68			
	Matches	57	Conservative	58	Mismatches	94
					Indels	84
					Gaps	16
QY	51	RQOQLKVDPRKRLQASLQITGVGVVYVSWAKVSKCEKMAQLSHYTTVLVLDSSDDPYAM	110			
DB	90	RSKRLIVAPREIQ-----QWFEITAQ-LTLD--HLPSIKFTDVNEXTRPQ	134			
QY	111	MNYENDIQAGREQAHPMWALVNEHPNVLRHGPFCSLNT-IRSLTDFEGGCMIAQVNF	169			
DB	135	LT--DELP--QANP-----LSHRVPEFARSIVYKIQKKID-----	167			
QY	170	GFPSGSHYPOFLRKRMNGCHCVGASLWKEQDFGLTLEITSALQWENMVMVWVNDLMS	229			
DB	168	-----IQVLTQGVSKG-DIWHL--KGVYVEEGRLKQDFKION--QQ	210			
QY	230	FYKEFDDERDOIISLVKNVYVDSDEITLHEA-----LEKLTQDTLHSSQMVAVPSDKDPQ	283			
DB	211	IHAITGGDNBRPELLADACKDAQQLIHATVLTQVLDVKGKQPMSSAMVAEFAEQ--Q	268			
QY	284	VMDITIECMHGVVWMLCDHRYRLNEIYKAKGQK--TEDAQPKFKFEQAN	334			
DB	269	SLDNL-----ILTHGSPR-----HODKTQQAITEVNGQFKKHNYLAN	307			

Query Match	4.3%;	Score 88;	DB 4;	Length 509;
Best Local Similarity	20.7%;	Pred. No. 1.8;		
Matches	63;	Conservative	44;	Mismatches 104; Indels 94; Gaps 17;
QY	14	VLLEIYIRYDSNYSREERIENLHYAYNKAHFAQPRQOQLKVDPRKLOASIQIYGM	73	
Db	14	IGLMNATTKCDHNNYSKNPMRIYCVYGTWSYH-----KVDPTIIDIDPFCKTH	63	
QY	74	VVYSMAVYSKECMAADLSIHYYTL-VLDDSSDDPYRAMNY-----FNDLQAGRQAHW-	127	
Db	64	LMYGFAKIDE-----YKYTIQVDFPQDDHNNWEKGYERFNNLRKNDLTTMI	114	
QY	128	-----MALVNEHFPVULHFGPFCSLNIRSLTDFEFCGIEWOYVFG-----FPGSH--	175	
Db	115	SLGSGWYSGSEKYSIDMAAN--PYTRQGVQSVYDF-----LQYKFDGLDLDWEYFGSKLG	167	
QY	176	-----DYEQFLRBMNGLGHCVGASLMPKEQDFERGLFLEITSALA-----	215	
Db	168	NPKIDKQNYLLIVREL-----KEAFEPFPYLL--TAAVSPGDKIDVAYELKELN	215	
QY	216	QMEHNM-----VVVNDL--MSFYKEEFDDERDOI SLVKNYVVSDEITLHEALEK-L	262	
Db	216	QLFPMNNVMTYDYHGGWENFQHNAPLYKR-PDETDELHYFNV-----NYTMHYLLNNGA	270	
QY	263	TQDTLL 267		
Db	271	TRDQL 275		

Search completed: December 9, 2004, 18:49:39
Job time : 29 secs

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OM protein - protein search, using sw model

Run on: December 9, 2004, 18:48:38 ; Search time 149 Seconds

(without alignments)
910.925 Million cell updates/sec

Title: US-09-710-760-2

Perfect score: 2050
Sequence: 1 MEMPREVFLNTSVRLLEYI.....DVDVKEIKQKPLLSIEIVE 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	6.3	440	US-10-448-871A-33	Sequence 33, Appl
2	107	5.2	725	US-10-156-761-9701	Sequence 9701, Ap
3	98	4.8	1564	US-10-389-566-1234	Sequence 1234, Ap
4	97	4.7	681	US-10-156-761-13818	Sequence 13818, A
5	96	4.7	1162	US-10-452-024-113	Sequence 113, App
6	95.5	4.7	763	US-10-424-599-192645	Sequence 192645,
7	94.5	4.7	781	US-10-425-114-49494	Sequence 49494, A
8	94.5	4.6	879	US-10-149-310-52	Sequence 52, Appl
9	94.5	4.6	1201	US-09-863-776-61	Sequence 61, Appl
10	94	4.6	514	US-10-369-493-6698	Sequence 6698, Ap
11	94	4.6	713	US-10-437-963-150539	Sequence 150539,
12	94	4.6	750	US-10-437-963-185546	Sequence 185546,
13	94	4.6	1107	US-10-032-585-7483	Sequence 7483, Ap

14	94	4.6	1460	9	US-09-815-242-13668	Sequence 13668, A
15	93.5	4.6	381	17	US-10-425-115-283715	Sequence 283715,
16	93.5	4.6	1053	17	US-10-425-115-345011	Sequence 345011,
17	93	4.5	346	14	US-10-012-819-82	Sequence 82, Appl
18	92.5	4.5	220	17	US-10-425-115-282876	Sequence 282876,
19	92	4.5	309	15	US-10-425-115-54740	Sequence 54740, A
20	92	4.5	327	15	US-10-424-599-154357	Sequence 154357,
21	92	4.5	411	15	US-10-425-114-64692	Sequence 64692, A
22	92	4.5	444	14	US-10-369-493-22063	Sequence 22063, A
23	92	4.5	1162	15	US-10-452-024-114	Sequence 114, App
24	91.5	4.5	880	15	US-10-149-310-50	Sequence 50, Appl
25	91	4.4	2326	14	US-10-369-493-6374	Sequence 6374, Ap
26	90.5	4.4	495	17	US-10-425-115-326239	Sequence 326239,
27	90.5	4.4	1469	14	US-10-369-493-5675	Sequence 5675, Ap
28	90.5	4.4	2861	14	US-10-374-979-108	Sequence 108, App
29	90.5	4.4	2861	14	US-10-374-979-108	Sequence 89, Appl
30	90.5	4.4	2861	15	US-10-182-936A-108	Sequence 108, App
31	90.5	4.4	2861	17	US-10-477-238A-687	Sequence 687, App
32	90.5	4.4	2861	17	US-10-680-287A-687	Sequence 687, App
33	90.5	4.4	3038	10	US-09-863-776-62	Sequence 62, Appl
34	90	4.4	729	14	US-10-094-749-2118	Sequence 2118, Ap
35	90	4.4	1162	15	US-10-452-024-115	Sequence 115, App
36	90	4.4	2100	14	US-10-195-144-59	Sequence 59, Appl
37	90	4.4	2100	14	US-10-345-072-59	Sequence 59, Appl
38	89.5	4.4	613	15	US-10-389-566-1884	Sequence 1884, Ap
39	89.5	4.4	623	15	US-10-389-566-1885	Sequence 1885, Ap
40	89.5	4.4	684	9	US-09-946-678-2	Sequence 2, Appl1
41	89.5	4.4	708	15	US-10-282-122A-66462	Sequence 66462, A
42	89.5	4.4	716	15	US-10-425-114-49283	Sequence 49283, A
43	89.5	4.4	763	15	US-10-424-599-192647	Sequence 192647,
44	89.5	4.4	765	15	US-10-149-310-38	Sequence 38, Appl
45	89.5	4.4	770	15	US-10-425-114-39704	Sequence 39704, A

ALIGNMENTS

RESULT 1
US-10-448-871A-33
; Sequence 33, Application US/10448871A
; Publication No. US20040093169A1
; GENERAL INFORMATION:
; APPLICANT: Mizushima, Yoshiyuki
; APPLICANT: Sakaguchi, Kengo
; APPLICANT: Sugawara, Fumio
; TITLE OF INVENTION: A METHOD FOR DESIGNING A MOLECULAR STRUCTURE OF AN INHIBITOR FOR
; FILE REFERENCE: 03316/LH
; CURRENT APPLICATION NUMBER: US/10/448, 871A
; CURRENT FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 33
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Simian foamy virus type 3
US-10-448-871A-33

Query Match 6.3%; Score 130; DB 15; Length 440;
Best Local Similarity 20.4%; Pred. No. 0.0013;
Matches 83; Conservative 66; Mismatches 142; Indels 116; Gaps 21;
QY 45 HHPA---OPROQLKVDKRLQASIQITGVNIVSWAVSKCMADLSIHYYTIVLD 100
DB 9 HHATGTGNRPKQYPIKPK-AKASIQIVINDLKGVLIIQONSINWTVYVP----- 61
QY 101 DSSDDPYPAMNNFENDLAQRE--QAHPPWALVNEHPVNLRFH--GPFSMLIRSTLD 156
DB 62 PKPDGKRWLVLD-----REVNKTIPLIADONSHAGLSSIFRCKY-----KTLLD 108
QY 157 FFGSCWIEQYFPGFSGHDYPOFLRRMNGLGCHGVGASLWPKSQPDERGULF-LEITSIA 215
DB 109 LSNQFMVHSHST-----PESY-----WLTAFTWLGGOYQYCWTRLPQGLNSPALFTADVLDLK 160

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QY 216 OMENMMWVNDLMSFKPEPDERDQI-----SLVKN--YVVS---DEITLHEA----- 258
Db 161 EYBNVGVYVDDI---YISHDDPREHLEOEKVFSLILNAGYVLSLKSSSIAGIEVFLGF 217
QY 259 -----LEKLTQDT-----LHSSKQWAVFSDSDPOVMDTIEGF 291
Db 218 NITKEGRGLTEFKQKLTNITPRDJKQLOSLIGLNFARNITPNFSELVKPLNITATA 277
QY 292 MHGYTWHLCDHRYRLNEIYEKYGKQ-----TEDAQKCFYEQAQANV 335
Db 278 NGKYIITW--TTDMSQQLNITISMLNSAENLEERNPEVRLIMKNVTPSAGYIRFY----- 330
QY 336 GAVSPSEWAPPPIAOLANIRSK--DYKDVADVK---EIOKPLISSTEL 378
Db 331 -----NEFAKRPIIMVNTYITAEVAFKFTTEKLTITTHKGLIKALDL 372

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RESULT 2
US-10-156-761-9701
; Sequence 9701, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9701
; LENGTH: 725
; TYPE: PRF
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9701

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Query Match 5.2%; Score 107; DB 14; Length 725;
Best Local Similarity 21.5%; Pred. No. 0.48;
Matches 62; Conservative 42; Mismatches 102; Indels 82; Gaps 15;

QY 88 DLSHYTYTLVLDSSDDPYRPMANNYFNDLQA-----GREGAHP----- 126
Db 441 DLSRW--LAWGTYGDDYPMVFGPRRDILAAKLCRRLSACMPVGBEVPANVGMER 497
QY 127 ---WMLVN-EHFPNVLRHGRCPSLNLIRSTLDFEGCWTIEQY--FGGFGSHDYP 178
Db 498 GLIDLMATTAEKTPDERRTF-----RASVDVTESVWELSNQLOHRIIDPIDYL 548
QY 179 QFLRRNG-----LGHCVGASLWPKQFDERGLFLRTISAIAMEN-----MMWVNV 225
Db 549 EMRATATGADLTLSLCVGH--GPKVPE-----YRSGVRLERNAADVGMILIN 597
QY 226 DLMSEYKEPDE--RQISLVKNYVVSDEITLHELEKLTQDTLHSSKQWVA-----VF 277
Db 598 DVFSYQKEIEYEGEVHNAIIVQNFPGCDYFTALGVINDIMTQRMHQFEHVAAREPLLY 657
QY 278 SD-KDPQ-----VMD-----TIECFMHGYVTWHLCDHRYRLNEIYEKYG 316
Db 658 KDFKLPQEVARDINDGYVEIQLNMWMSGILKWHQDCHRYGAADLARRAHG 705

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RESULT 3
US-10-389-566-1234
; Sequence 1234, Application US/10389566

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; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52500)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1234
; LENGTH: 1564
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-10-389-566-1234

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Query Match 4.8%; Score 98; DB 15; Length 1564;
Best Local Similarity 21.0%; Pred. No. 11;
Matches 87; Conservative 59; Mismatches 108; Indels 160; Gaps 25;

QY 7 EYFLNTSVRLLEYIRYRDSNYTREERIENLHVAYNKAHHFAQPRQOQLKVP----- 60
Db 844 EYDSSSVKNIVLTRYQSEDSRSSTWETR-----AQAREKEWEDPGLRME 892
QY 61 -----KRLQASLQTVGVNVVSMKVSKECMADSIHTYTLVLDSSDDPYPM 110
Db 893 KLENKAEONQKDKKSPAQIDITRLISYKVN--ASSGH-----LQOQSRNETYPS- 944
QY 111 MNYFNDLQAGREQAHPWMLVNEHFPNVLRHFGPCSLNIRSTLDF--PEG---CW-- 162
Db 945 SEVFHVRRTG-----TNSNYSAYTR-----SKLDFHFPSGDRVDWLP 983
QY 163 -IQYNGFGFPESHY--PQFLRRNGLGHCVGASL-WPKQEPDERGLFLEITSAIAMEN 219
Db 984 KLEQF-----FSLDTPBELKVSIASTLCDGAALKYSLF-----ESDPGVXLGN 1030
QY 220 MWWW-----VNDLMSFKPEPDERDQISLVKNYVVSDEITL 255
Db 1031 KMYKLLBSHPAEVLDDPISLKKQKXTNGIIEYHKFELLRARVNSEDYLV----- 1084
QY 256 HEALEKLTQDTLHSSKQW--VAVFSDKDPQVMDTIECFMHGYTWHLCDHRYRLNEIYEKY 314
Db 1085 ---RVYLDGLHPDTQNMVNMF--QPQTV---CQCLLVG-----RLYEGV 1120
QY 315 KQKQT-----EDAQKCFYEQAQANVAVS---PSEWAPPPIAOLANIRSKD 358
Db 1121 H-QKILIRKVGDERK-----GAPTLNVPNEVAGP---SLSNIHVD 1159

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RESULT 4
US-10-156-761-13818
; Sequence 13818, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30

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PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 13818
 LENGTH: 681
 TYPE: PRT
 ORGANISM: Streptomyces avermectilis
 US-10-156-761-13818

Query Match 4.7%; Score 97; DB 14; Length 681;
 Best Local Similarity 21.6%; Pred. No. 4.1;
 Matches 81; Conservative 56; Mismatches 138; Indels 100; Gaps 20;

QY 61 KRLQASLQITVGM-----VYSMAKVSKECMADLSIHYYTLVLDDSSDDPYPA 109
 DB 41 QRLASFFQDLAHPRTTRVTTAASVETWSTVEBA-LQLESWIKEXD-----PR 92
 QY 110 MMVYFNDLQAGREQAHPMAL-VNEHPPNV-----LRHGPFCSLNLRSTLDPF 158
 DB 93 FNVKVRD-----DKSYPLAVTMBEFPVQVWGHKRGKRYRGFGHMAIRDTVDL 147
 QY 159 -----EGCWIEQYNG-----GPGSHDYPOFLRRMNGLGHCVGASLMPKEQFDE 203
 DB 148 LRVFVPTCSAGYFNKNAARTGRPCLTGIGKSNP-CVERVSAEHEBELA-----BEFCD 201
 QY 204 -----RGFLFETLSIAQEMENMMVNDLMSFYKEFDEDRDQISLVKNYVSDDEI 253
 DB 202 FMAGRTGTJYIRLEROMTDAEEME-----YKKAARLRDIDIGALKAMEKNAY 249
 QY 254 TLHEA-----LEKLTQDTLHSSKQWAV-----FSPDKDPQVMDTIECFMNGYVTHLCDHRY 305
 DB 250 VLADATDADILAAVEDELEAAVOIFHYRGGRVAGQGRWVTDKVE-----ATTADLVGH-- 303
 QY 306 RLNEIYEVKVGQKTEDAQKCFEYBOANVAVSP-SEMAVPIAQLANIRSKDVXDKVD 364
 DB 304 ALQOLY-----GEETGDSVP--KEVLVPALPDPVPEVQEWLTGRRGSIVSLRIPQGRDKS 357
 QY 365 VKE-IQKPLLSITEL 378
 DB 358 LMETVORNAQOSLAL 372

RESULT 5
 US-10-452-024-113
 Sequence 113, Application US/10452024
 Publication No. US20040013687A1
 GENERAL INFORMATION:
 APPLICANT: Simpson, Lance
 APPLICANT: Park, Jung-Beak
 TITLE OF INVENTION: Compositions and Methods For Transendothelial Molecular Transport
 FILE REFERENCE: 9855-9601
 CURRENT APPLICATION NUMBER: US/10/452,024
 PRIOR FILING DATE: 2003-06-02
 PRIOR APPLICATION NUMBER: 60/384,949
 NUMBER OF SEQ ID NOS: 188
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 113
 LENGTH: 1162
 TYPE: PRT
 ORGANISM: Clostridium botulinum
 US-10-452-024-113

Query Match 4.7%; Score 96; DB 15; Length 1162;
 Best Local Similarity 16.5%; Pred. No. 11;
 Matches 79; Conservative 72; Mismatches 143; Indels 184; Gaps 20;

QY 9 FLATSVALLIYIR-----YRDSNYTTEERIENLHYA--- 39
 DB 77 FLQATIKLQRIINNNAVGAKLISLSTAIIPFYENNTEDYRQTVLSSKNNHYYTANLV 136
 QY 40 -----YVKAHHFAPQRRQQL-----KVDRRLQASLQITIVGM 74

DB 137 IFPGSNIKNVIYKK-----EVAESGMGTLMIEWPQPLTHKYDERVYVPALELI----- 189
 QY 75 VYSMAKVSKECMADLSIHYYTLVLDDSSDDPYPAMMYTNDLQAGR----- 121
 DB 190 -----KLIK-SLYLYYGIKPNDNLNIPY-RLNEBNSLEYSELNIDFLISGID 238
 QY 122 ---EQAHPMALVNEHPPNVLRHGPFCSLNLRSTLDPFEGCMIQYNGFPGSHDYP 178
 DB 239 YKLNTPYV-FIDKTFIDTSKNP-----EKI-----KNDYB 269
 QY 179 QFLRRMNGLGHCVGASLMPKEQFDERGLFLEITSAIAQEMENMMVNDLMSFYKEPD--- 235
 DB 270 IKIKNNNYANSI-----KLYIEQGFKNVND--IMELNLSYFSGEFDIM 313
 QY 236 -----DERDQISLVKNYV---SPEITLHEALEKLTQDTLHSSKQWAVFS 278
 DB 314 PERYNALNHYRKEFVVIDYFKQYVINGKNGQIKTKPLSKYKKEIINKPELIVNLIN 373
 QY 279 DKQPOVW-----DTIECFMNGYVTHLCDHRYRLNEIY-----EKVQKQKT 319
 DB 374 QNNTVLMKSNYGDGLKGVNDNFYSNLIIPYNLNYEHSINVFYLDVNVIEIEKIPIND 433
 QY 320 ED-----AQKCFEYE--QAANVGAVSPSEMAVPIAQLANIRSKDVXDKVKEI 368
 DB 434 EDIYPRKXADTPIPVNITKAKEINTTPLPVNY---LQAMIDSNIDNLSDBFLKV 488

RESULT 6
 US-10-424-599-192645
 Sequence 192645, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovalic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 192645
 LENGTH: 763
 TYPE: PRT
 ORGANISM: Glycine max
 OTHER INFORMATION: Clone ID: PAT_MRT3847_15981C.1.pcp
 US-10-424-599-192645

Query Match 4.7%; Score 95.5; DB 15; Length 763;
 Best Local Similarity 21.1%; Pred. No. 6.8;
 Matches 95; Conservative 69; Mismatches 135; Indels 151; Gaps 27;

QY 11 NTSVRLLEYIRYRDSNY-----TREERIENLHYVNRQAHHFAPQRRQQLKVDPRKLQAS 66
 DB 101 NATVPAMEKTKWPDYTHFIPELIGDVPNTVASHKAVDEY---KEAKALGVD-----T 151
 QY 67 LQTIIVGVVY-----SMKVS-----KECMADLS-----HYTY-TLV 98
 DB 152 IPVAVGPVYVLLSKPAKGVKSFSLSLPKVLAYKVEYIAIDAKAAGASWIDQDEFTLV 211
 QY 99 LDDSS-----DDPYPAMMYFNDLQAGREQAHPMALVNEHPPNV-LRHGPFCSLN-- 149
 DB 212 LDLSHSLQAFDTAVALAPALSDLN-----VLVETYPADIPABAAYKTLTSLNGV 261
 QY 150 -----LIRS--TLDPFEGCMIQYNGFPGS-----SHDYPOFLRRMNG 186
 DB 262 TAYGFDLVRGTHLTDLIK-----GGFPGSKYVLAGVVDGRNIVANDLAASLTTLQG 312
 QY 187 LGHCVGASLMPKEQFDERGLFLEITSAIAQEMENMMVNDLMSFYKEFDEDRDQISLVKN 246

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Db      313 LEGIVG-----KDK-----LVSTSSSLHTAVDLVNE-----TKLDE-----IKS 349
Qy      247 YV--VSDDEITLHLEKLTQDTLHSSKQWAVFS-----DKDPQVMDTIECFMNGY 295
Db      350 WIAFPAQKIVEVNAALAKAL-----SGNKVAFPSANAAAQASRKSSPRV--TNEAVQKAA 402
Qy      296 VTMHLCDHRYRLNEIYEKVGQKTEDAQKFCFYEQAANVGAV--SPSEWAPPIAQLANI 354
Db      403 AALKSGDHR--RATNVASRL-----DAQ-----QKKNLPILPTTISFPQVVELRRV 449
Qy      355 R-----SKDVADVADYKEIQKPLLSIEIIVE 380
Db      450 RREFRANKISEEYVKSIEIKRIVELQOE 479

RESULT 7
US-10-425-114-49494
; Sequence 49494, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Jingdong
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 49494
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700834118_FLI.pep
US-10-425-114-49494

Query Match      4.7%; Score 95.5; DB 15; Length 781;
Best Local Similarity 21.1%; Pred. No. 7.1;
Matches 95; Conservative 69; Mismatches 135; Indels 151; Gaps 27;

Qy      11 NTSVRLLEYIRYRDSNY-----TREERIEHLHYAANKAHHPAORQOQLKVDPRQLQAS 66
Db      119 NATVPAMEMTKMPDTNNHFIVPELGPVDNFTYASHKAVDEY---KEAKALVD-----T 169
Qy      67 LQTVGMVY-----SWAKIS-----KECMADIS-----IHATY--TLV 98
Db      170 IPIVAGPYTYLLLSKPAKGVESFSLSLPRKVLAVYKEVIADIKAKAGASWIGDEPFLV 229
Qy      99 LDDSS-----DDPYRAMNVEFNDLQAGREGAHPMMLVNEHPNV--LRHGPFCSLN-- 149
Db      230 LDLESHKLGATDVAEIAEAPALSDLN-----VLVETVADITPAEAKTKLTSLNGV 279
Qy      150 -----LIRS--TLDFEGCWIIEQYNFGGPPG-----SHDYPCQLRRMNG 186
Db      280 TAYGFDLVRGTHHTDLIK-----GGFSGKYFLFAGVVDGGRINMANDLASLTLLQG 330
Qy      187 LGHVUGASLWPKBQFDERGLFLEITSAIQEMNMWVNDLMSYKFPDDERDOISLVKN 246
Db      331 LEGIVG-----KDK-----LVSTSSSLHTAVDLVNE-----TKLDE-----IKS 367
Qy      247 YV--VSDDEITLHLEKLTQDTLHSSKQWAVFS-----DKDPQVMDTIECFMNGY 295
Db      368 WIAFPAQKIVEVNAALAKAL-----SGNKVAFPSANAAAQASRKSSPRV--TNEAVQKAA 420
Qy      296 VTMHLCDHRYRLNEIYEKVGQKTEDAQKFCFYEQAANVGAV--SPSEWAPPIAQLANI 354
Db      421 AALKSGDHR--RATNVASRL-----DAQ-----QKKNLPILPTTISFPQVVELRRV 467
Qy      355 R-----SKDVADVADYKEIQKPLLSIEIIVE 380

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Db      468 RREFRANKISEEYVKSIEIKRIVELQOE 497

RESULT 8
US-10-149-310-52
; Sequence 52, Application US/10149310
; Publication No. US20040077039A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; APPLICANT: Madden, Kevin T.
; APPLICANT: Maxon, Mary
; APPLICANT: Sherman, Amir
; TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
; FILE OF INVENTION: Zinc Binuclear Cluster Proteins
; FILE REFERENCE: 14184-019US1
; CURRENT APPLICATION NUMBER: US/10/149,310
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US01/29288
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 60/233,564
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-149-310-52

Query Match      4.6%; Score 94.5; DB 15; Length 879;
Best Local Similarity 19.0%; Pred. No. 10;
Matches 80; Conservative 67; Mismatches 127; Indels 147; Gaps 23;

Qy      34 ENLHYAANKAHHPAORQOQL-----KVDPRQLQASL-----QTVG 72
Db      306 ONLKLFQKNSNSEBPDQALIDVFVNIIBRSLPASVINKTLAPRNEBSMRPSMQLQ 365
Qy      73 MVTYSNAKYSKECM-----ADLSIHYYTLVLDSSDDPYRAMNVEFNDLQAGRE---Q 123
Db      366 LRTYS--SDLEPELVDTIIPKTDLTVHGLARFLN-----HYENNVDKMTVVVLE 413
Qy      124 AHPMMLVNEHPFNVLRHFGPFCSLN-----LIRSTL-----DF 157
Db      414 KNNWKTLL--YFRALMALGDLAGQSSNSRNALLNALLAVSCHFLOSKYPRNYLQKX 470
Qy      158 FEGCWIIEQYNFGGFPESHDYPOFLRRMNGIHCQVGASLWPKBQFDERGLFLEITSAIQM 217
Db      471 FLGIIGIELRN-----QASNFLRLCLNT-----KSIPEK--YKQVLTAISM 510
Qy      218 ENMMWVNDLMSFYKFPDERDOISLVKNYV-----VDEITLHLEKLTQD 265
Db      511 -----NSIDVVGTMADQDHLACEDFVESRMKLRPNISEKKTTHRIFSPKLTQD 563
Qy      266 TLH-----SSKQWAVFSDKP--QVMDT-----IECFMNGYVTMHLCDHRYRLN 308
Db      564 STRLDKVRKKEIYLPSEEDDNYKPLDINATSSSSSPRVDDVQGL-----FREALN 616
Qy      309 EIEYEKVGQKTEDAQKFCFY--EQAANVGAVSPSEWAPPIAQLANISKDVADVKE 367
Db      617 E-----NDGKIHFVKEPITNVSAOSTPSTPPI--FNNIATESYNNKSDISN 664
Qy      368 I 368
Db      665 I 665

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RESULT 9
US-09-863-776-61
; Sequence 61, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A

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Qy      362 -----VKD---VKEIQKPLL-----SIEIVE 380
Db      614 SVSFHTHVXELMTWLELQLKELLDDVYASVEAVQ 648

RESULT 10
US-10-369-493-6698
; Sequence 6698, Application US/10369493
; Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6698
LENGTH: 514
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-6698

Query Match          4.6%; Score 94; DB 14; Length 514;
Best Local Similarity 20.9%; Pred.No.5.4;
Matches   43; Conservative 40; Mismatches    81; Indels   42; Gaps    9;

Qy      214 IAQMENMMVVNDLMSEFYK----EPDERPDISLVKNVVSDEITTLHEALEKLTPDTLLH 268
Db      267 LQMKRCVYYEGEHLFFHQFDMVDVGIDGRVFVYMPTTICHELDESPLMEIGADDLK 326

Qy      269 SSR-QMVAVFSDKDPQMDITEC--FMHGVTMLCDHRYLNEIYEKVKGQTEDAOK 324
Db      327 SAFAETILLEGVESVSGTTQARTSYLPSELW---GHRFEKLHYKKENGQNVIDRGG 383

Qy      325 FCKFY-----EQANVGAVSPEEW-AYPEIAQLANIRSKD---VKDYKYAE 367
Db      384 FHNVYSVNTPTCSAAIERLRSEGIFNBSERYOMYPSPDNKLTLLDNDEMSPVRSDIDLNQ 443

Qy      368 I-OXPLL-----SIEIVE 380
Db      444 VPQITLRDSDEDPPAGEESWEIVD 469

RESULT 11
US-10-437-963-150539
; Sequence 150539, Application US/10437963
; Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OR INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 150539
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(713)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_50766C.1.pep
US-10-437-963-150539

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Query Match          4.6%; Score 94; DB 16; Length 713;
Best Local Similarity 22.1%; Pred. No. 8.7;
Matches 74; Conservative 44; Mismatches 113; Indels 104; Gaps 18;

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QY 18 EYIRYRDSNYTREERIE-----NLHYAVNKAHFAQPR----- 51
DB 378 ESVKRYRDNLSRKRKEFEIIAOEGITCELPYDVCTRNSTYLMNAFPMRAVASLA 437
QY 52 -OQQLKVDPRKLSLOTIGMVVYSMAKVSKECMADLSHYTTVLVDSSDDPYPM 110
DB 438 VDDKNYKTAAPSPDQWERSTTVSGI-----LKVLYDATMVGSL---YPTS 480
QY 111 MNYPNDLQAGREQAHPW-----ALVNEHPNVLRHFGPFCSLNLRSTLDPFEGCMIQY 166
DB 461 NLYF-----HEMKIKLVLDKEHSNNDTE-----VASMQKKDKDKYMLASY 524
QY 167 NFGGFGSHDYPOFLRRNM-----GLGHCVGASLMPKEQDFE-----RGLFLEIT----- 211
DB 525 KILCLIPVLEF-D-PRF--KRFVFEFRLGQAFCEN--AKERIDKVKRMNMLFKESPDKLD 579
QY 212 --SALAOMENNM-VWVNDLMSFYKEPDERDOI SLVKYVVSDEITLHAEKLTQDTLH 268
DB 580 NANPLRQAEHVAISENDPMADW-EFGNKFDTLNMWKT-----NHSKYPTLACIAQDVLA 633
QY 269 SSKQNV-----VFSD-KDQVNDTIECFM 292
DB 634 WPASTVASESAFSTGSRVYSDPRCSLTWDSYEALI 668

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RESULT 12
US-10-437-963-185546
; Sequence 185546, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 185546
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_82431C.1.pep
US-10-437-963-185546

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Query Match          4.6%; Score 94; DB 16; Length 750;
Best Local Similarity 18.8%; Pred. No. 9.3;
Matches 77; Conservative 69; Mismatches 133; Indels 130; Gaps 20;

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QY 12 TSVRLLEYI-----RYRDSNYTREERIEINLHYAVNKAHFAQPRQQLKVDPRKLSL 67
DB 267 TSNQNLQYMCVLVAHYIIEENWMOCRVLN-----FIEVDPPH----- 302
QY 68 QTIQVMVVSMAKVSKECMADLSHYTTVLVDSSDDPYPMANVFNDOAGGEQA-HP 126
DB 303 ---TGIVY---AQAQVECMWEMKIEDKVTITLDDNATNNDTAATNLAKALLAKNSVFD 356
QY 127 WVALVN--EHFPNVLRFHG--PFCSL-NLIRSTLDPFEGCMIQYVNGFGPFGSHDYPOFL 181
DB 357 SYFHIRCAAHIVNLVNDGLQPIDNLISCLRNTVYKFKRSPRNY-----KFV 404
QY 182 RRNNGLGHCVGASLMPKEQDFERGLFLEIT---SALAOMENNMVWVNDLMSFYKEP--- 235
DB 405 EVCKNNYSVKG-----RGLADVCTRNSTYKMLDTCIDYKDAFGYKEVDTSY 453
QY 236 ---DERDOI SLVKYVVSDEITLHAEKLTQDTLHSSQMVAVFSDKDPQVNDTIECF 291
DB 454 VMKPSDDWVSFGK-----IRPIQTAEAATAFSG---SLYFRANCF 493
QY 292 MHGYVTWMLCDHRYRLNEIYKVGQXTEDA-----QKFKFYEQAAVAVSP- 340
DB 494 -----YPIYVVKRALIEAQSEBDTYLRSGAAMLDFDKYWEKKNVVIAT 542
QY 341 -----SEWAYPPIAQLAN-IRSKVDVVDVKEIQKRLSIEIV 379
DB 543 LDPRFKRYIKWCF--AQLFPDICE--IEINDINOELRLYKYEIL 586

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RESULT 13
US-10-032-585-7483
; Sequence 7483, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Buseey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7483
; LENGTH: 1107
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7483

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Query Match          4.6%; Score 94; DB 14; Length 1107;
Best Local Similarity 21.6%; Pred. No. 16;
Matches 68; Conservative 50; Mismatches 127; Indels 70; Gaps 12;

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QY 66 SLQTIQVMVVSMAKVSKECMADLSHYTTVLVDSSDDPYPMANVFNDOAGREQAH 125
DB 27 SLKEVNTIKYDMPQMLRE---DANPIEVAVALDQTSVG-LAHLQERFMKESSEQA- 81
QY 126 PMWALVNEHPNVLRFHGFPFCSLNLRSTLDPFEGCMIQYVNGFGPFGSHDYPOFLRRNM 185
DB 82 -LRSVNEHYDLEFNKSWG---SYNTLLSTMKNSQDSLEIKX-----FLVYSN 125
QY 186 GLGHCVGASLMPKEQDFERGLFLEITSALAOMENNMVWVNDLMSFYKEPDERDOI SLVK 245
DB 126 -----KEYNDRAVAIVGEISSASAKTSE-MIEVLDMPEMNEIPGKIDQULVIDK 172
QY 246 N-YVVSDEITL-HEALEKLTQDTLHSSQMVAVFSDKDPQVNDTIECFMHGYVTWMLCDH 303
DB 173 KIHEVYDVISEGYTAEXKYNLMSLPAMNGIKTYLBEQSKLFDWIIDELQ----- 222
QY 304 RRLNLEIYKVGQXTEDAQKCFYEQAQVAVSPSEWAYPPIAQLANIRSKVDYK 363
DB 223 ---NEIYK-----YNNRPOEGAL-----AWONTIHSSNPQLTSGFVTL 258

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QY 364 DUKEIOKPLLSIEL 378
DB 259 DSKNLEQIFINSANL 273

RESULT 14

US-09-815-242-13668

Sequence 13668, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlson, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 13668

LENGTH: 1460

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-815-242-13668

Query Match 4.6%; Score 94; DB 9; Length 1460;

Best Local Similarity 19.3%; Pred. No. 24;

Matches 89; Conservative 71; Mismatches 180; Indels 120; Gaps 22;

QY 1 MENPTEYPLNT-SVRLLEYIRYSDSVYTRERIEHLHYAVYKAAHHFAQPRQOQLKVD 59

DB 306 MNNFTRLTYNVOQVGEVYERKDLMPGERRAVE--FHAHTNSTDALPEVEEIVATA 363

QY 60 PK-----RLQASLQTVGM-----VYSMAVVSCEM 86

DB 364 AKWGHKAVAITDHGNVSPFGYKPAKAGIQLYGMENANIVEDRVIVYN-----EVE 417

QY 87 ADLSIHYYTLVLDDSSDDPYPAMMYNFNDLQAGR-----EQAHPMNA--- 129

DB 418 MDL-LEATY--VVDVETTGISAIYNDLIQVAAKMKYKGVIAFDEFINPGLSAFTT 474

QY 130 -----LVNEHPN-----VLNHFGRFC-SLNLIRSTLDFEGCWIEOYNFGFP----- 172

DB 475 ELTGITDHDVNAKPLQGVLFQGFCDITLVVAHNATFDVGFNNANYERHGLPKISQPV 534

QY 173 -----GSHDYPOPLRKNNGIHCVC---GASLMPKEQDERGLPBLITSAIQMENMVM 223

DB 535 IDTLFPAANLYPEYK--HGIGPLTKRFGVAL---EHNNMANYDAEATGRLL-----FIF 584

QY 224 VNDLMSFYKEFDDBDOISLVKNTVVSDEITLHEALEKLTQDTLHSSKOMVAVFSDK--- 280

DB 585 IKEYAEKHGVTDLARLNLIDISPDYSYKARIKHAITYYKQVGLKNIKLVLSLNTKTFE 644

QY 281 -DPQVMDTI-ECFMHGYVTMHLCDHRYRLNEIYERKYGOKTEBDAQECKPEQOANVAV 338
DB 645 GVPRIPTVDAHREGLIISGACSE---GEVFDVAVSGVDNAVAKITD---FIEVM 657

QY 339 SPSEMAVPIAQLANIRSKVDVKEIOKPLLSIEL 378
DB 698 PPAIYA-PLIAK-----EQVKMEELQITIKSLIEV 727

RESULT 15

US-10-425-115-283715

Sequence 283715, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

PRIOR FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 283715

LENGTH: 381

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_21847C.1.pcp

US-10-425-115-283715

Query Match 4.6%; Score 93.5; DB 17; Length 381;

Best Local Similarity 21.7%; Pred. No. 3.9;

Matches 49; Conservative 30; Mismatches 66; Indels 81; Gaps 10;

QY 166 YNFGGFRGSHDY--QFLRMNGIHCYAGASLMPKQFBERG---LFLITSAIAQEMW 220

DB 4 FNFTEGP---FPLGPFLLNRRTIRTEAVKGSILFPEQOALGFSSYSTNIRMTVTKSG 59

QY 221 MVMVNDLMSFYKEFDDBDOISLVKNTVVSDEITLHEALEKLTQDTL-HSSKOMVAVFSD 279

DB 60 GLWVHAPIATKTC-----IQWLKE-----LAPVENVILPFFAYEHKIFVGEFSR 105

QY 280 KDPQVMDTIECFMNGYVTMHLCDHRYRLNEIYERKYGOKTEBDAQECKPEQOANVAVS 339

DB 106 KFPKAO-----IW-----VA 115

QY 340 PSEMAVPIAQLANIRSKVDVKEIOKPLLSIEL 378

DB 116 PROMSWPILNPLEFFGIFRAKPLKDBDDATPWVAIEQKVLSSPEV 161

Search completed: December 9, 2004, 19:00:41
Job time: 152 secs

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